

FIG. 1

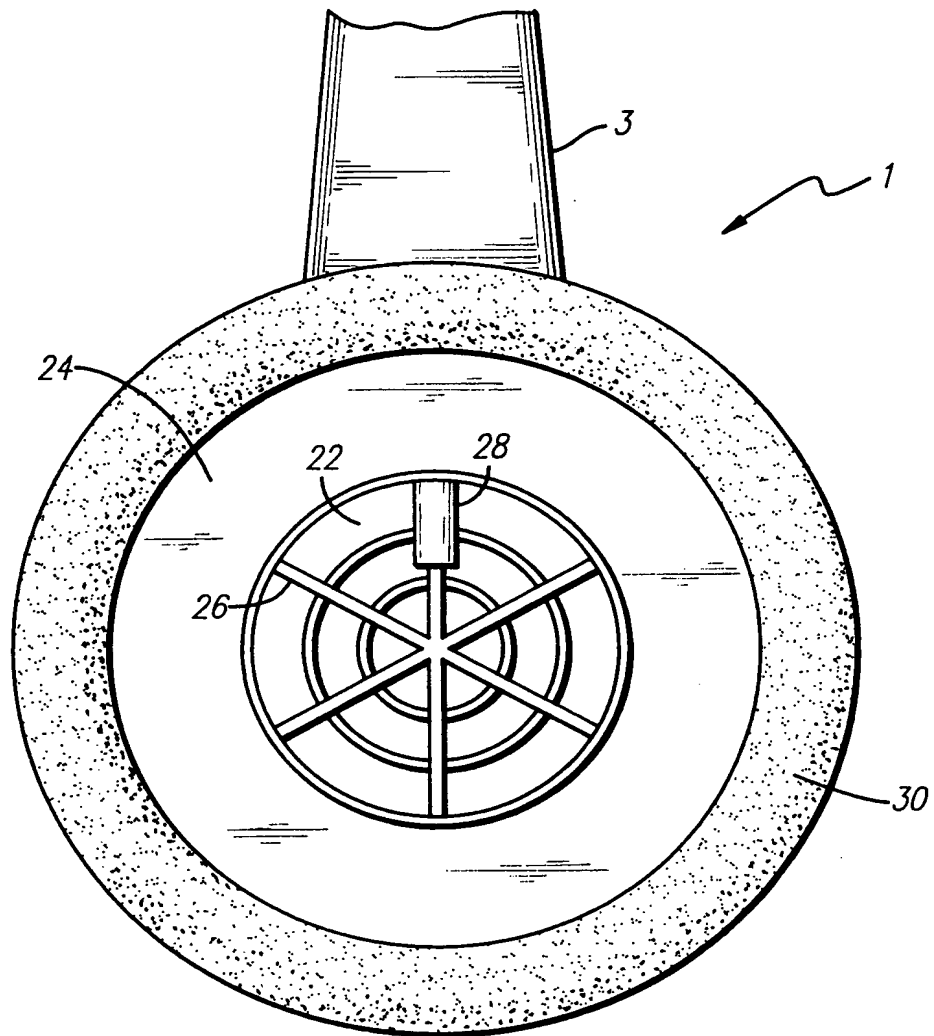


FIG. 2A

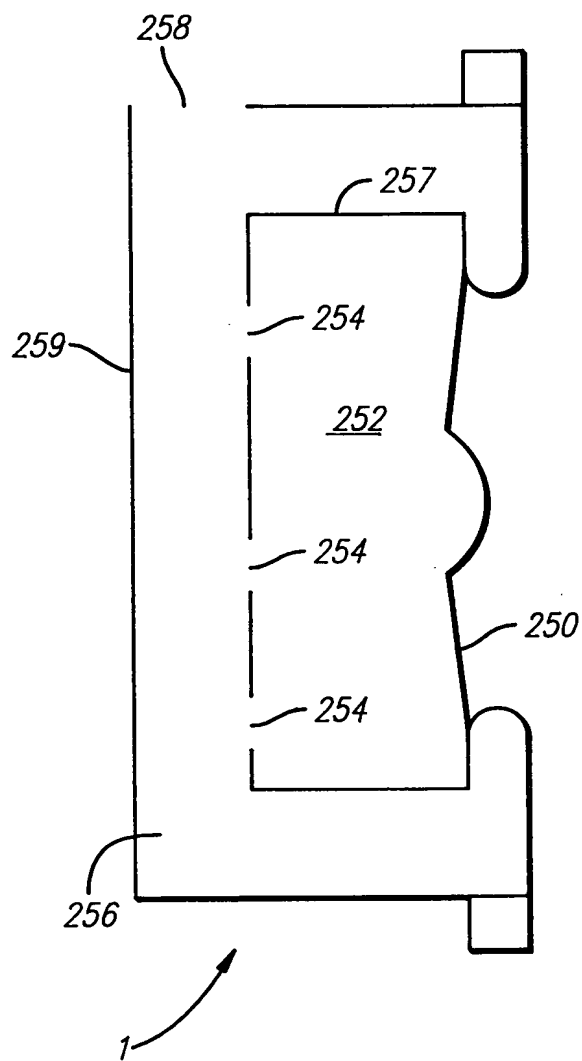
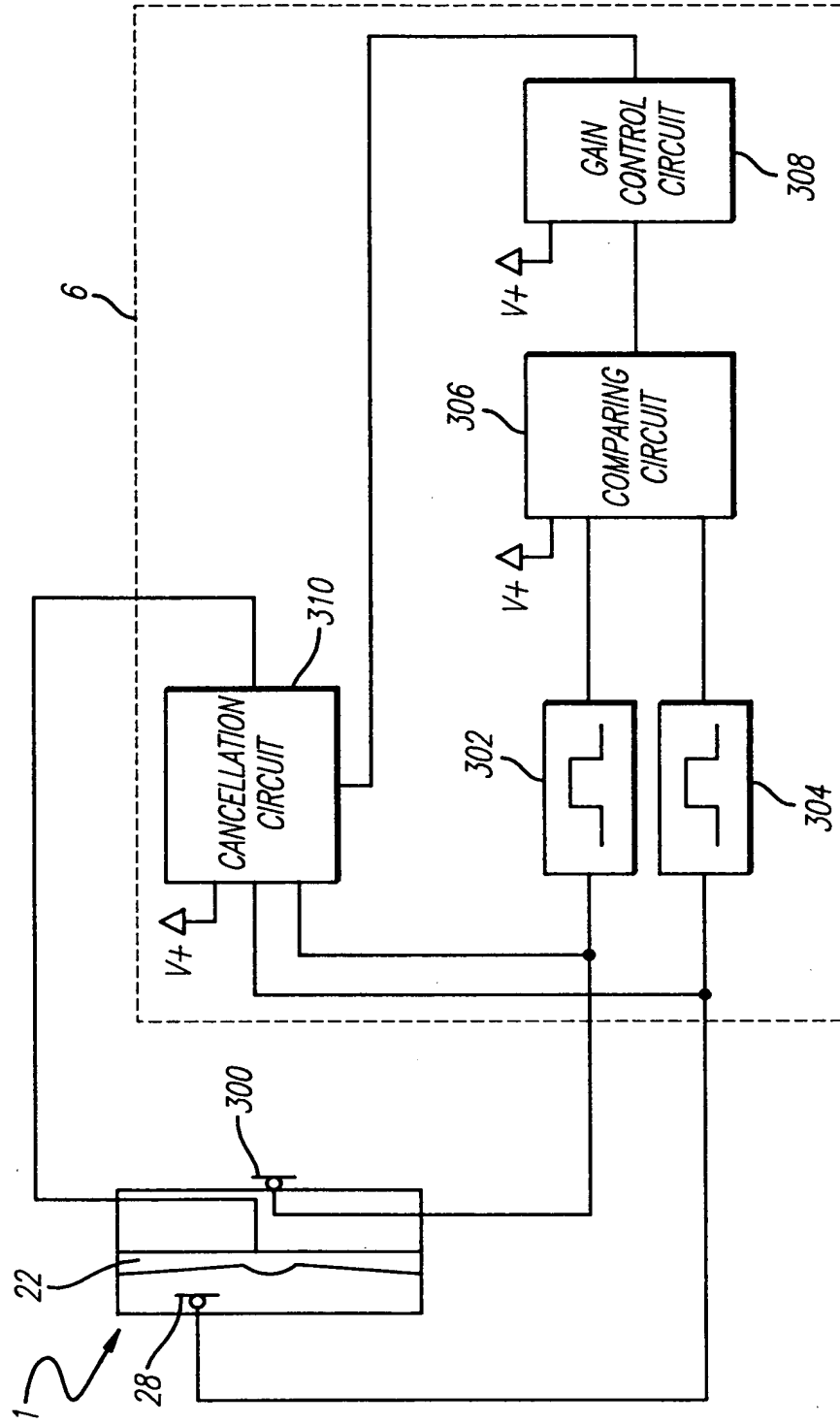


FIG. 2B

[illegible]

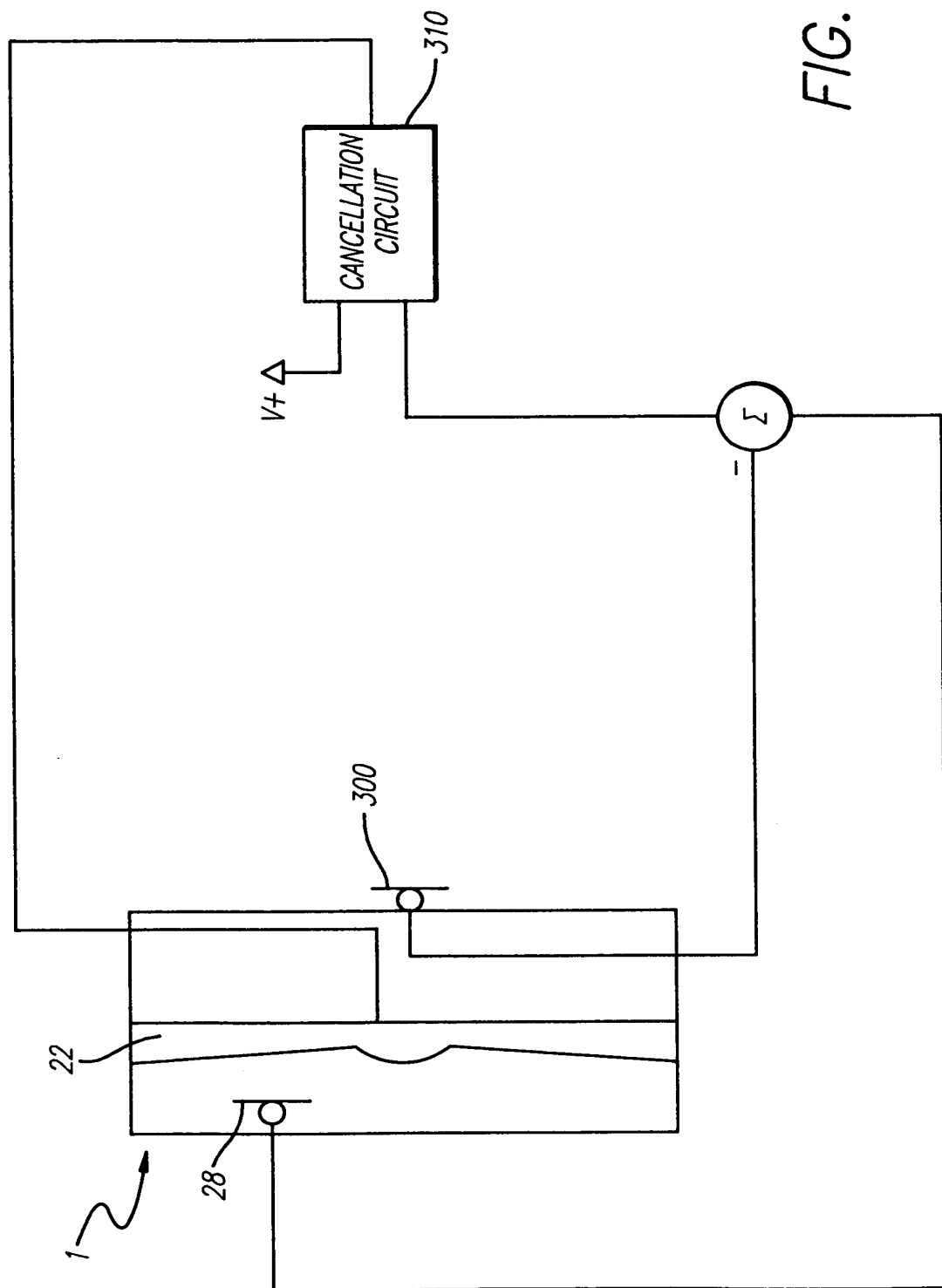


FIG. 3A

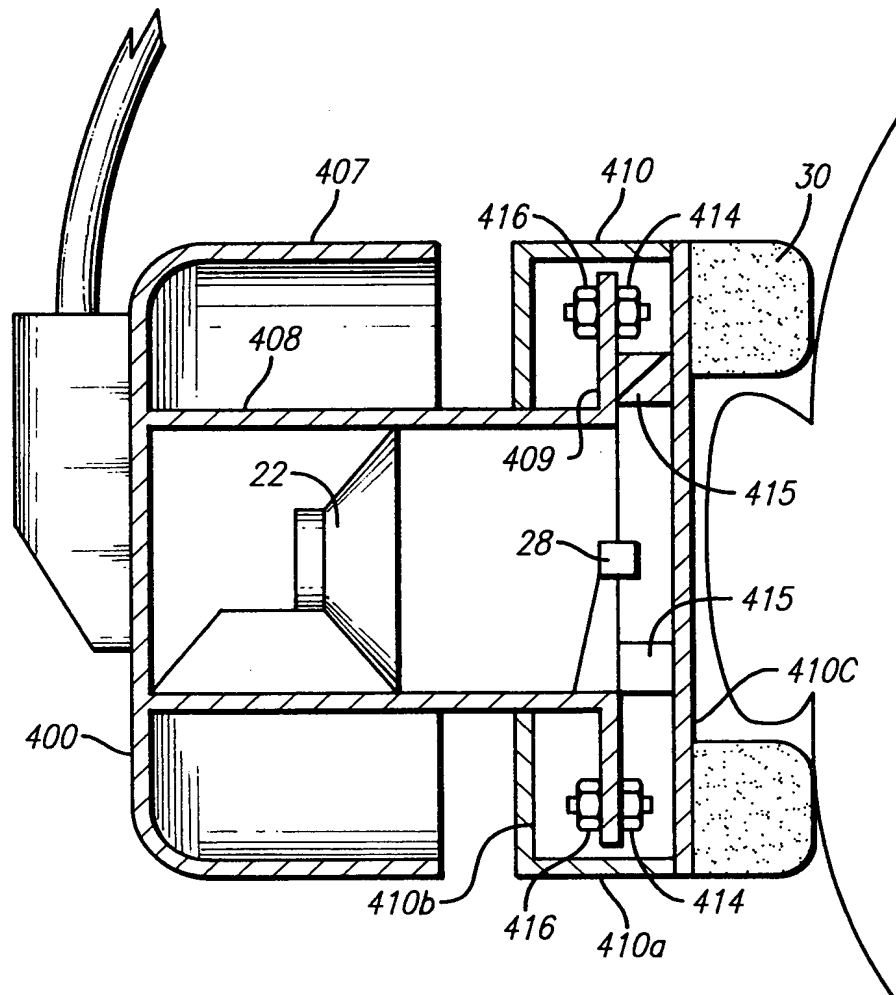
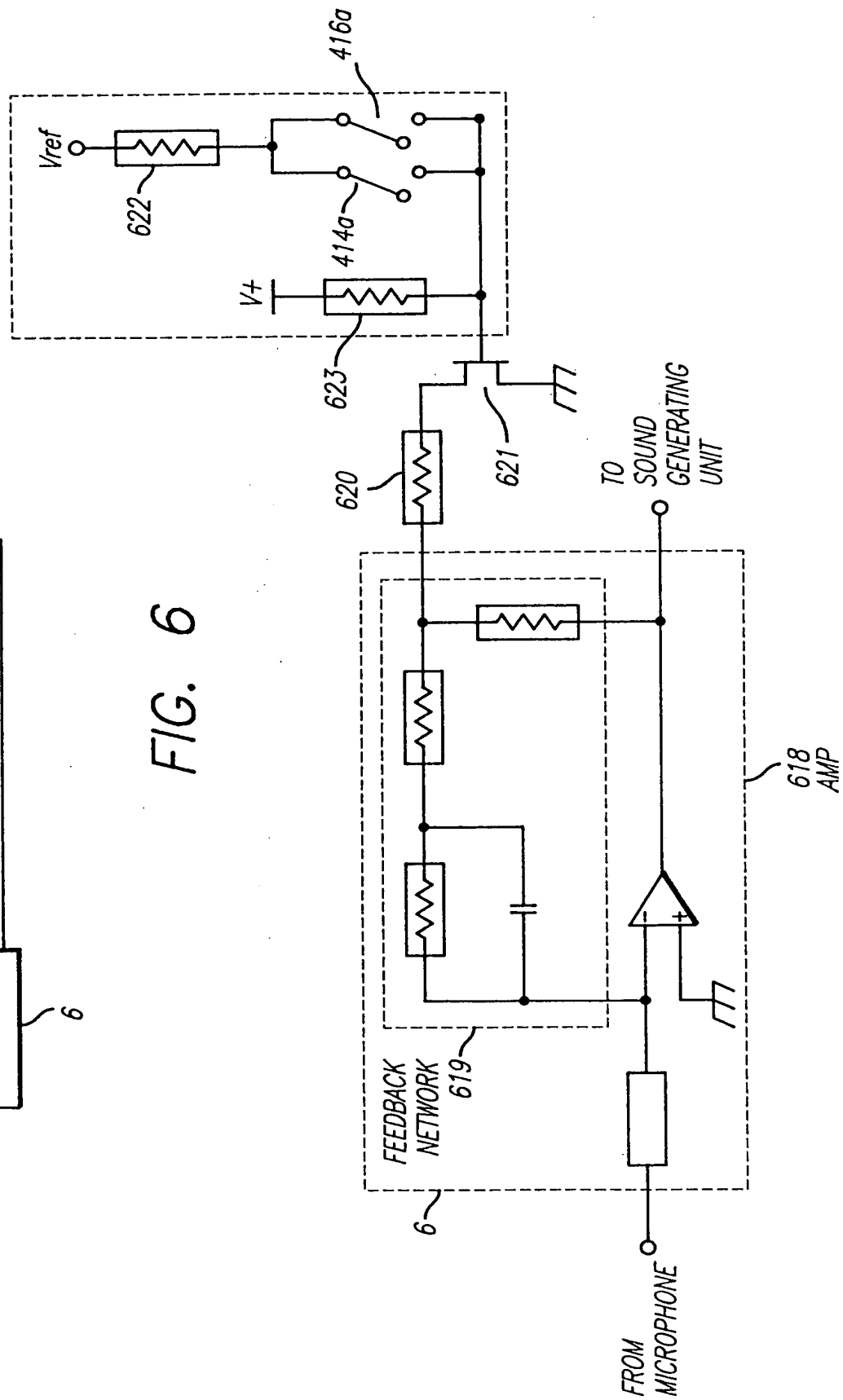
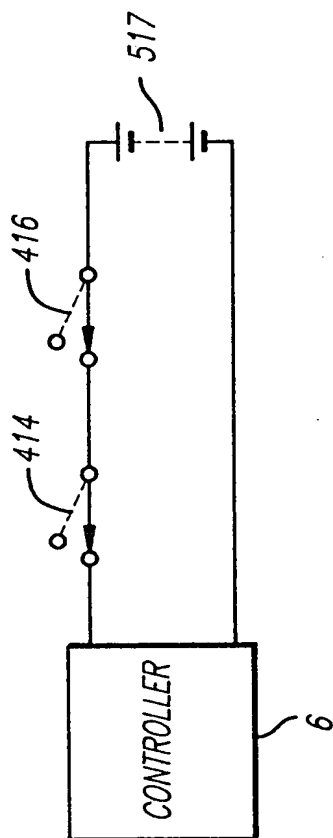


FIG. 4



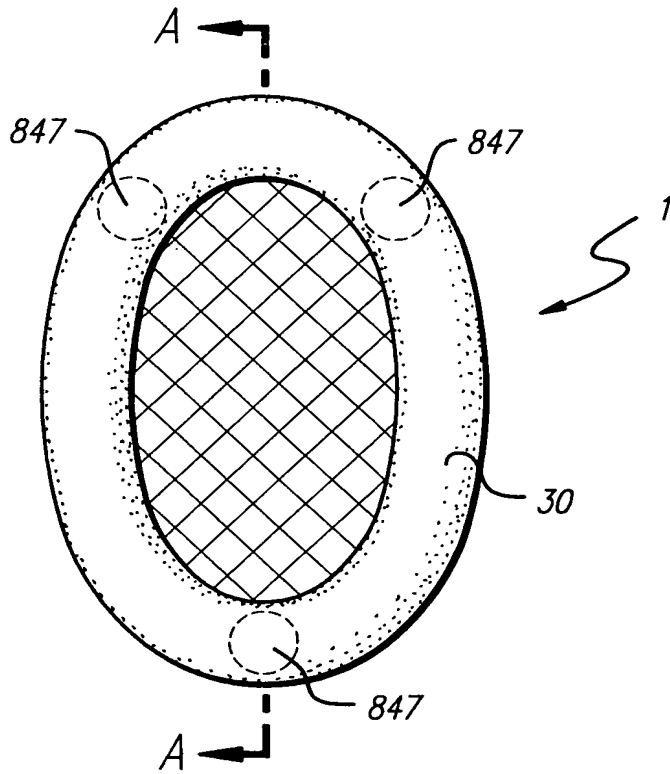


FIG. 7

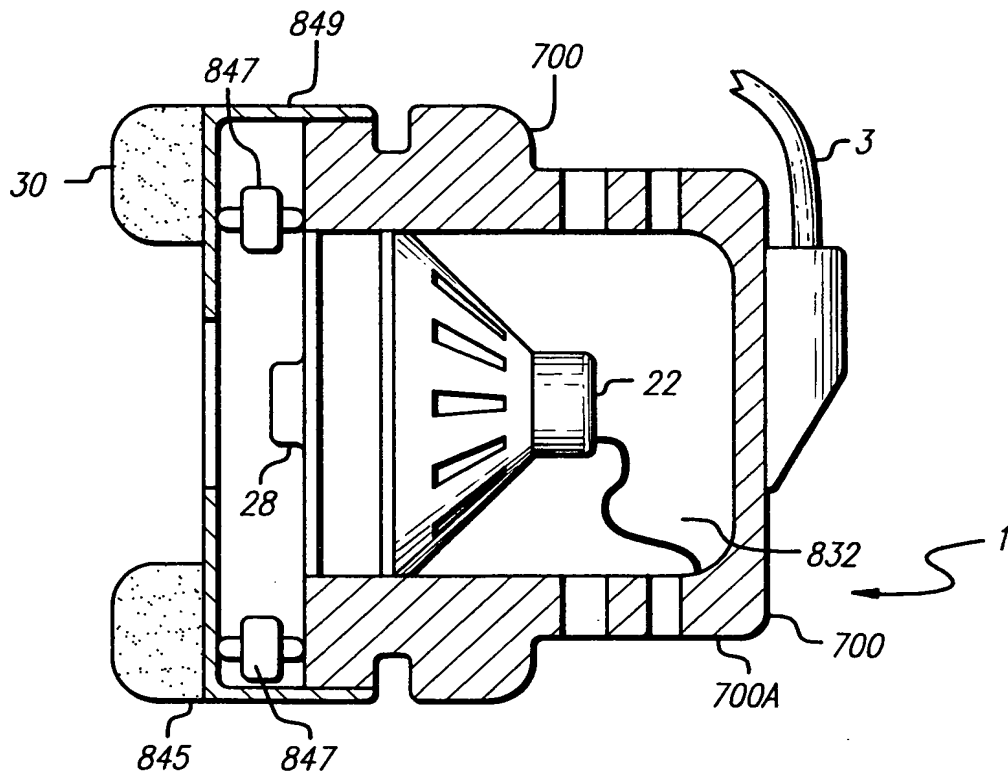


FIG. 8



1. *Phylogenetic relationships* among the studied taxa were determined using the maximum parsimony method. The analysis was performed using the software package PAUP 4.0 (Felsenstein, 1999). The heuristic search was conducted using 1000 random taxon addition and 1000 iterations of branch swapping. The support for the nodes was assessed using 1000 bootstrap replicates. The parsimony-informative characters were identified using the program Mesquite 2.0 (Maddison & Maddison, 2005).



FIG. 9B

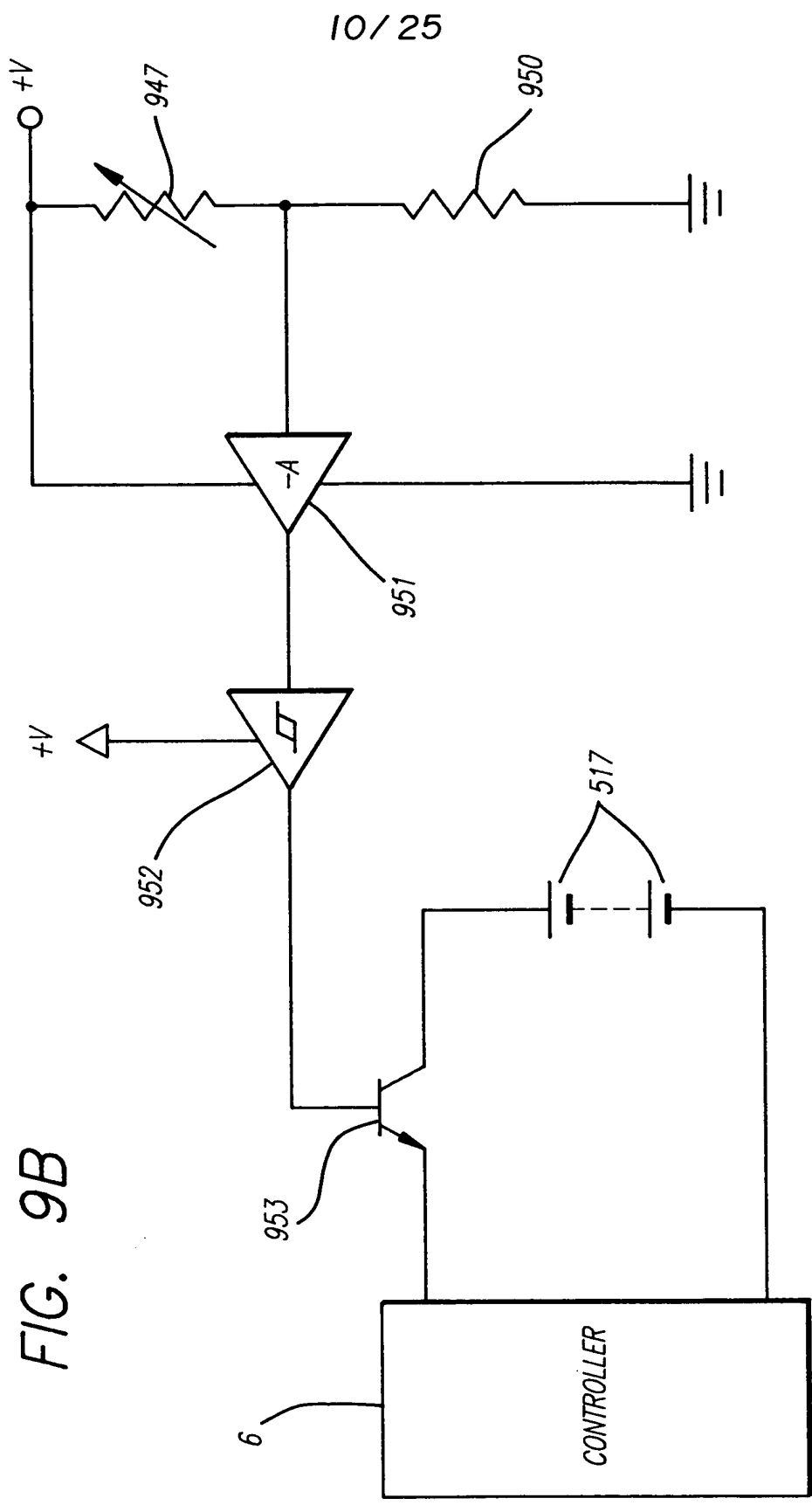
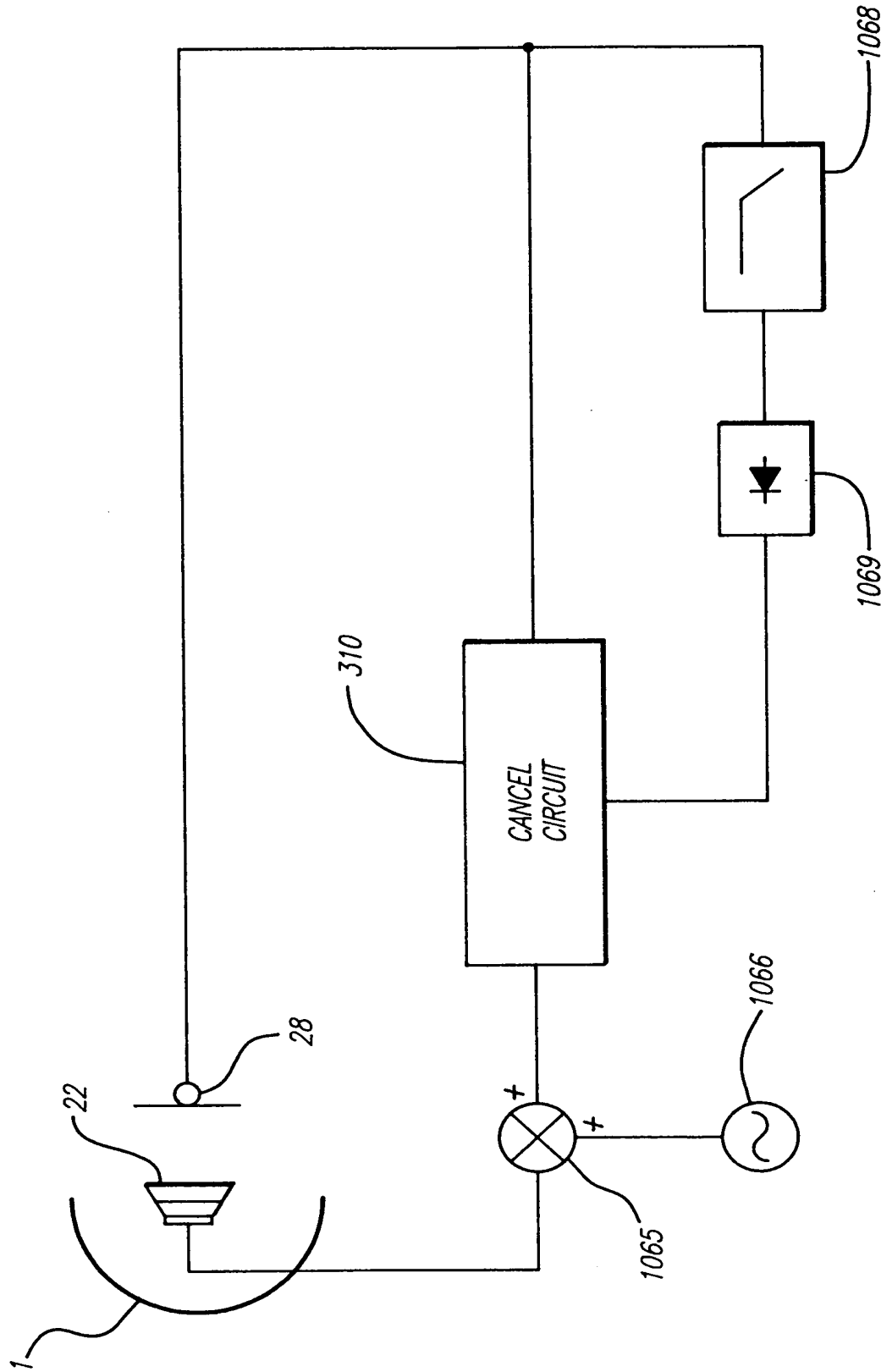


FIG. 10



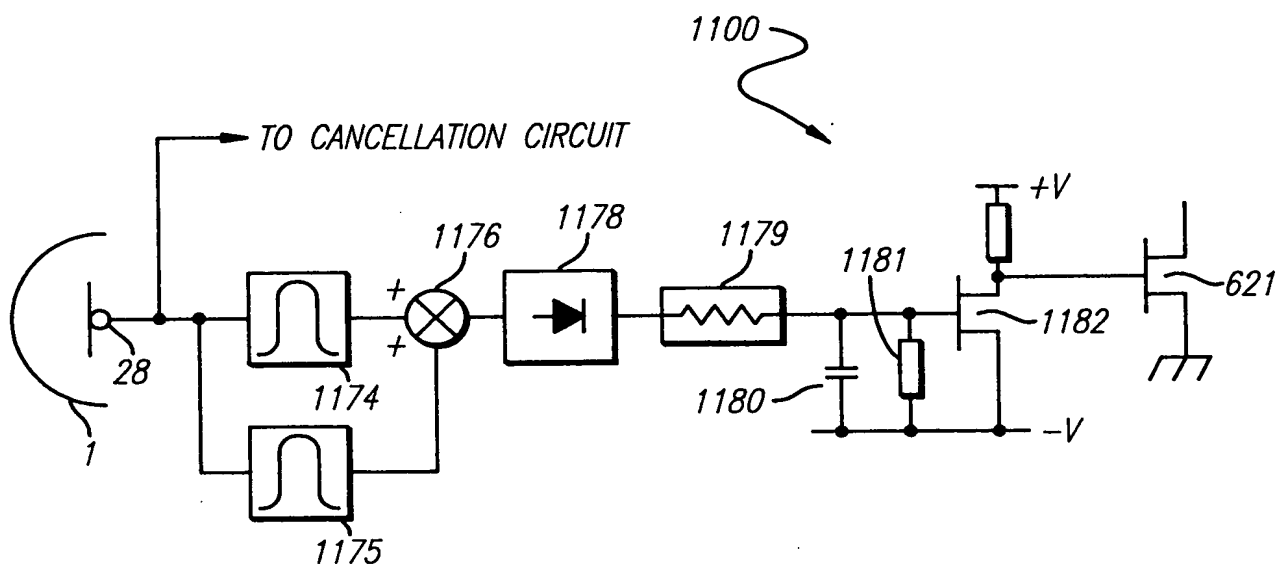


FIG. 11

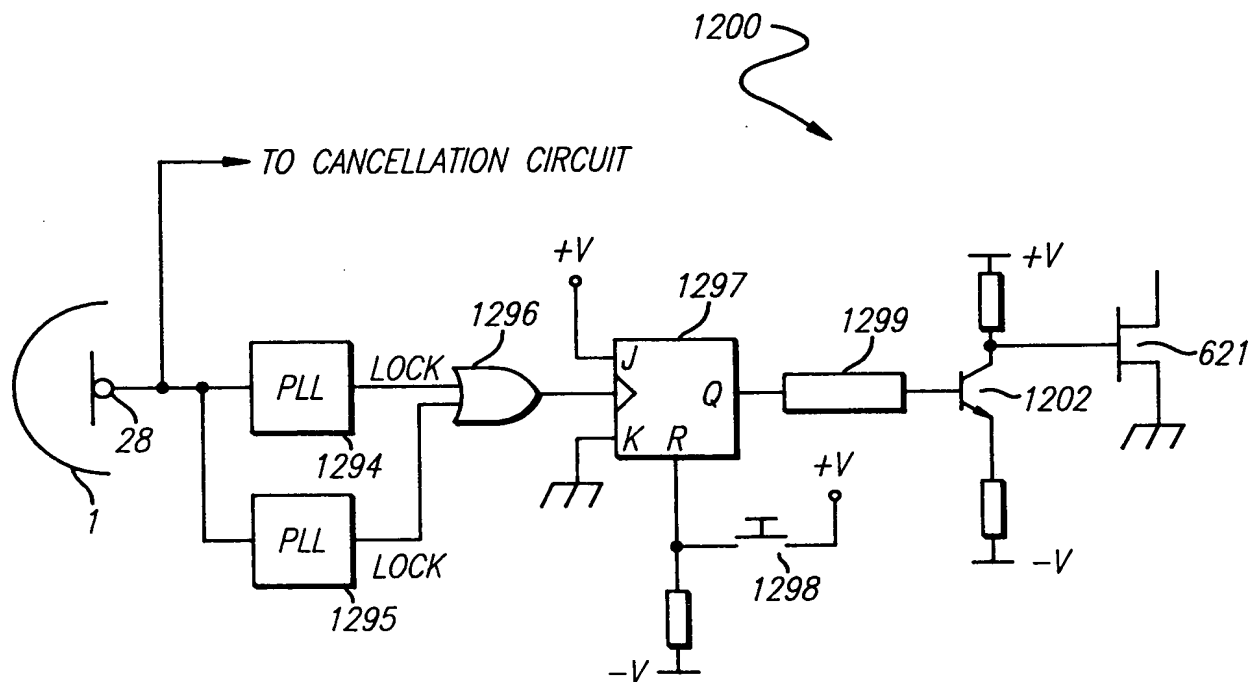


FIG. 12

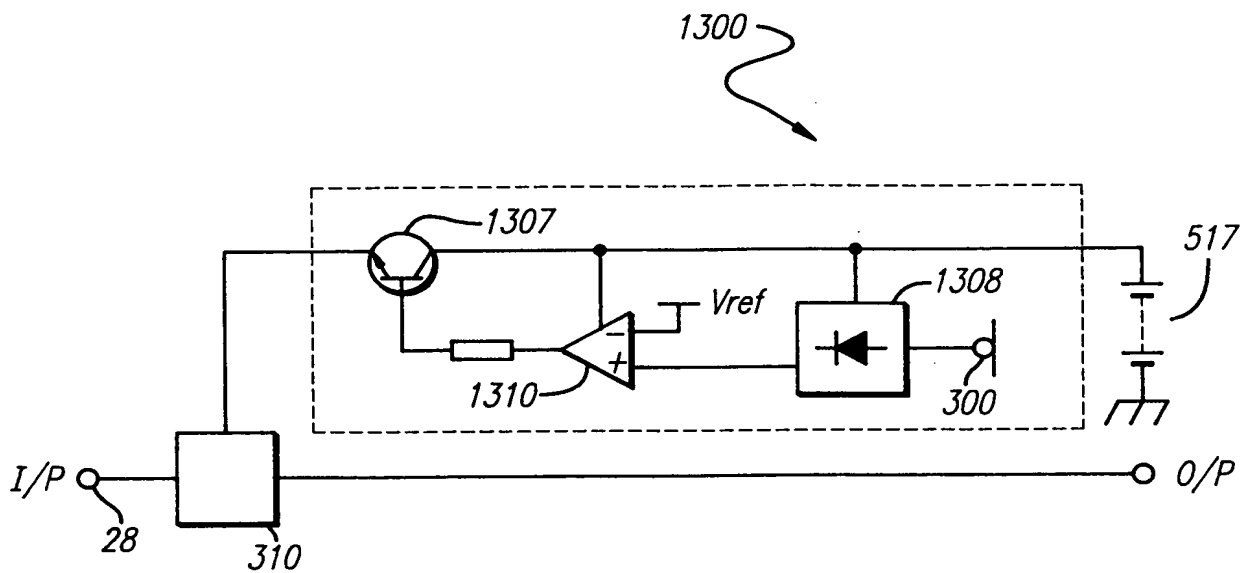


FIG. 13

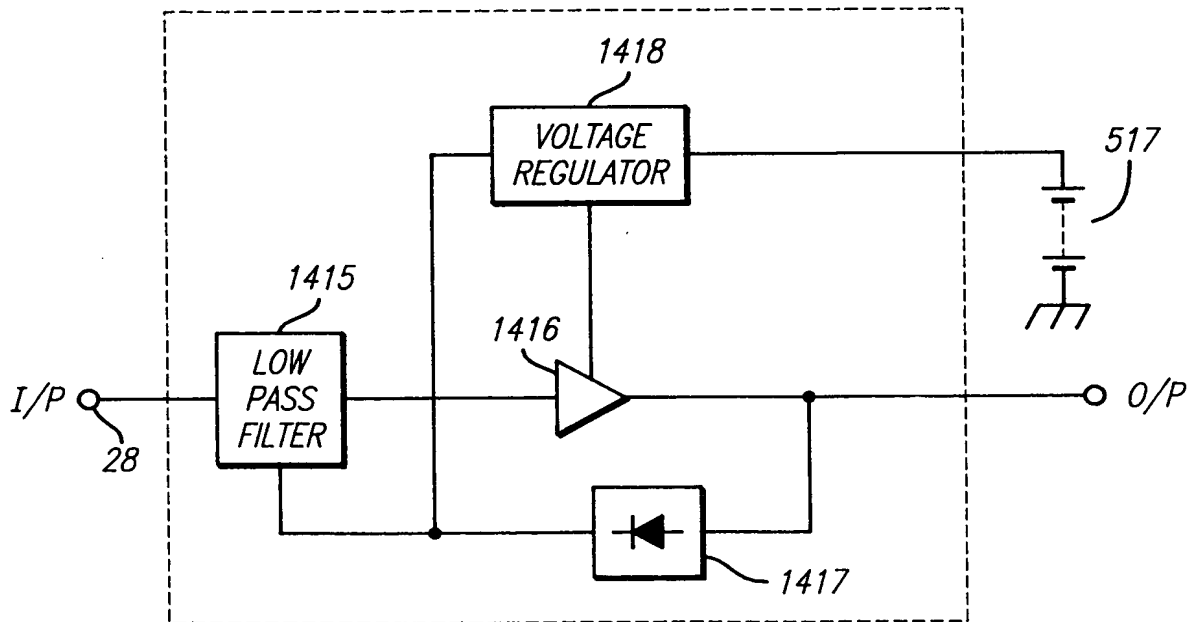


FIG. 14

FIG. 15

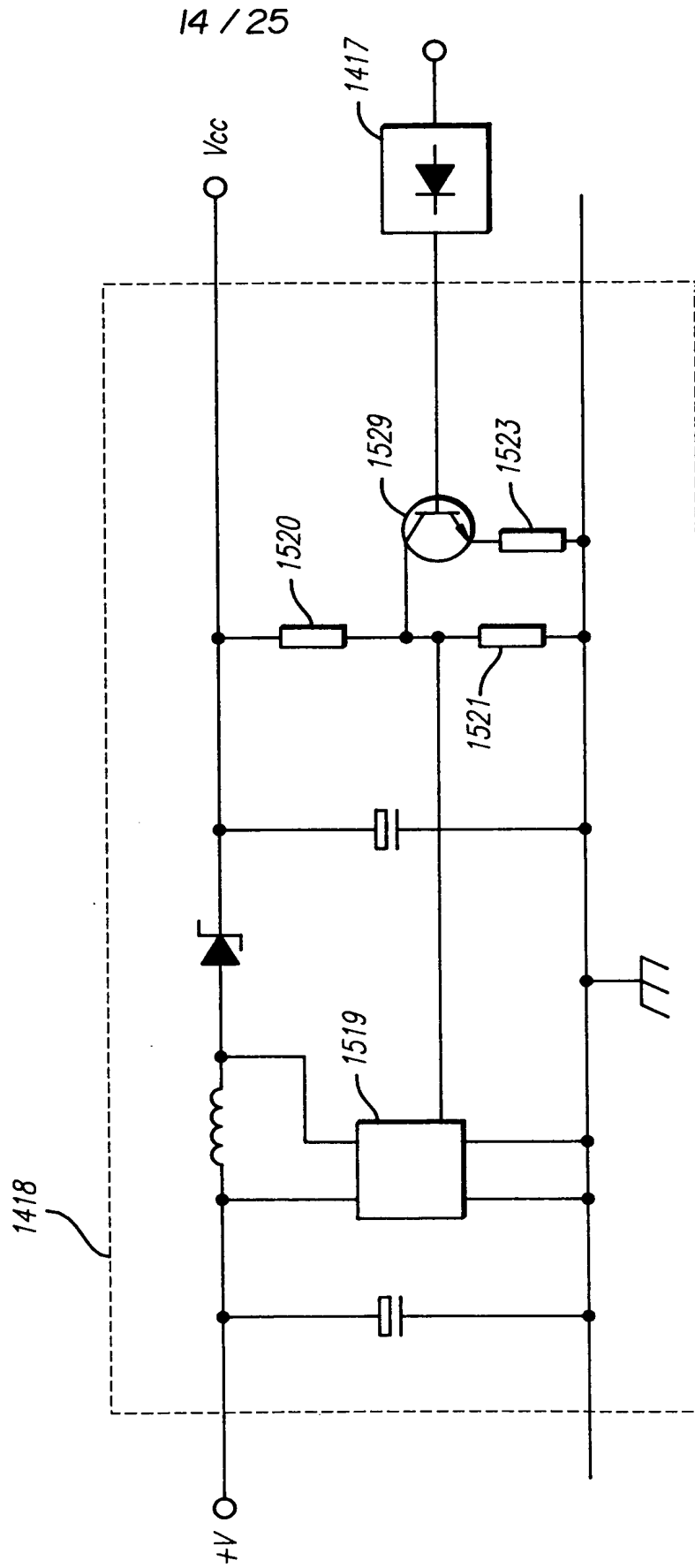
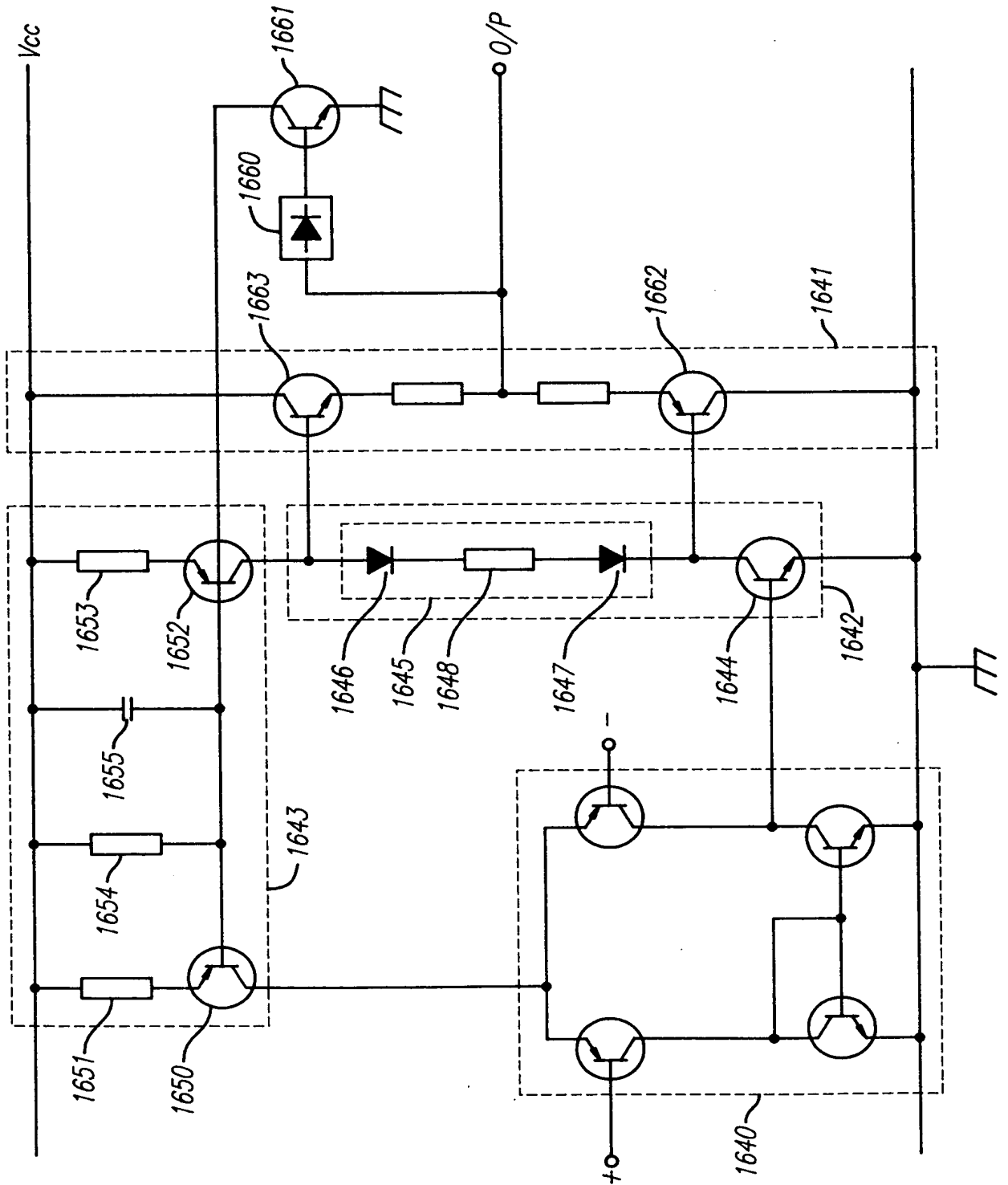


FIG. 16



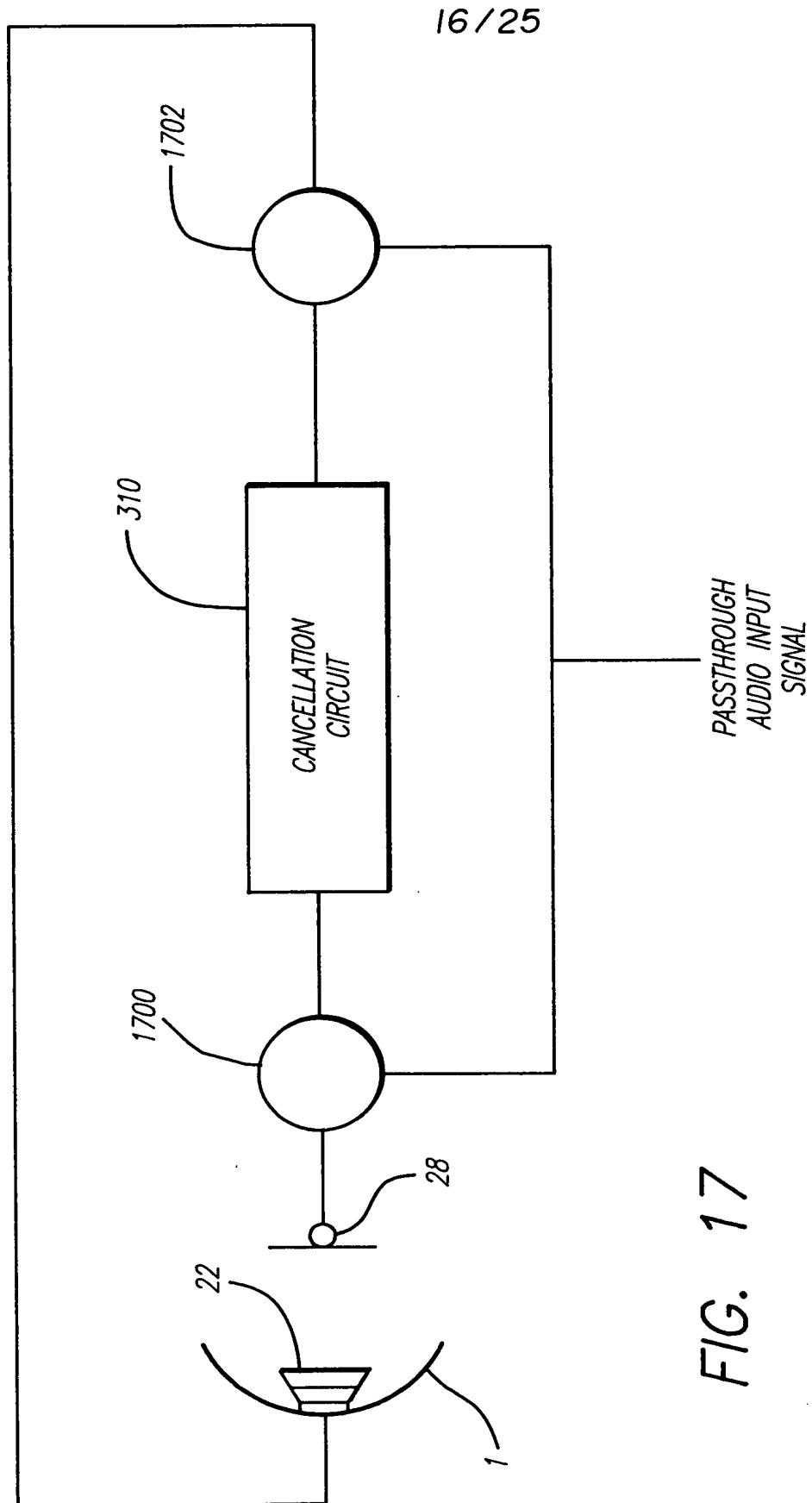


FIG. 17



FIG. 18

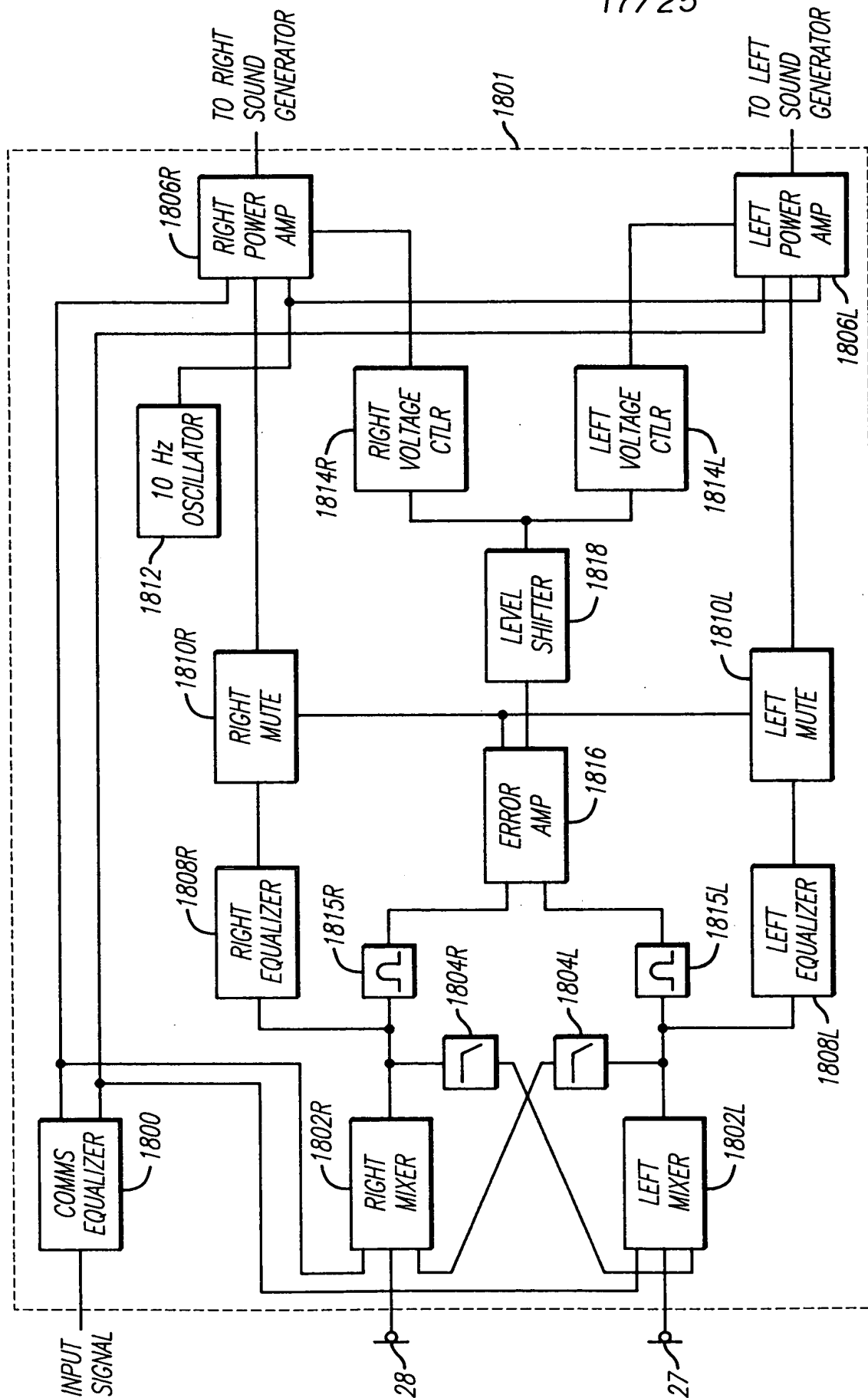
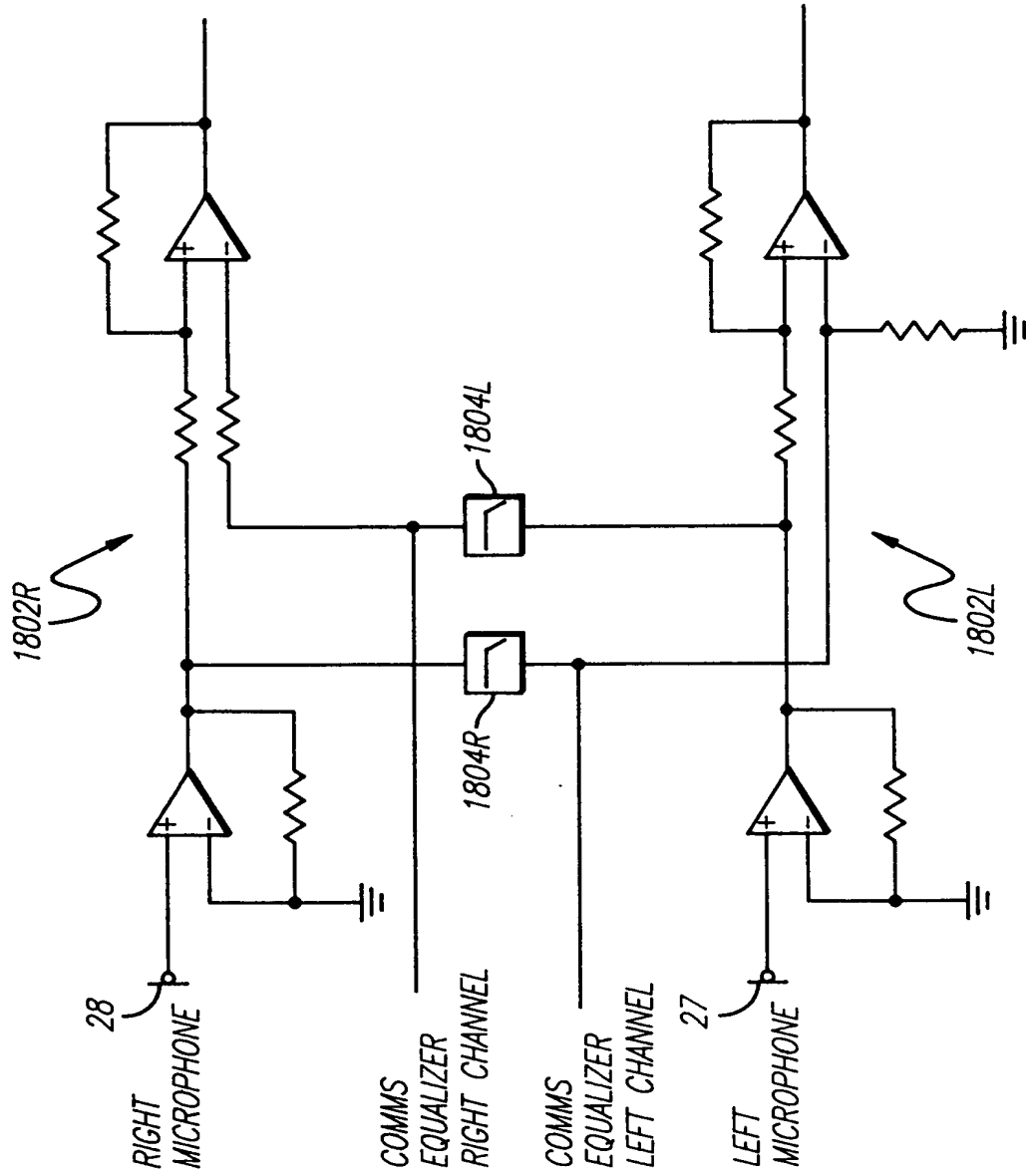


FIG. 19



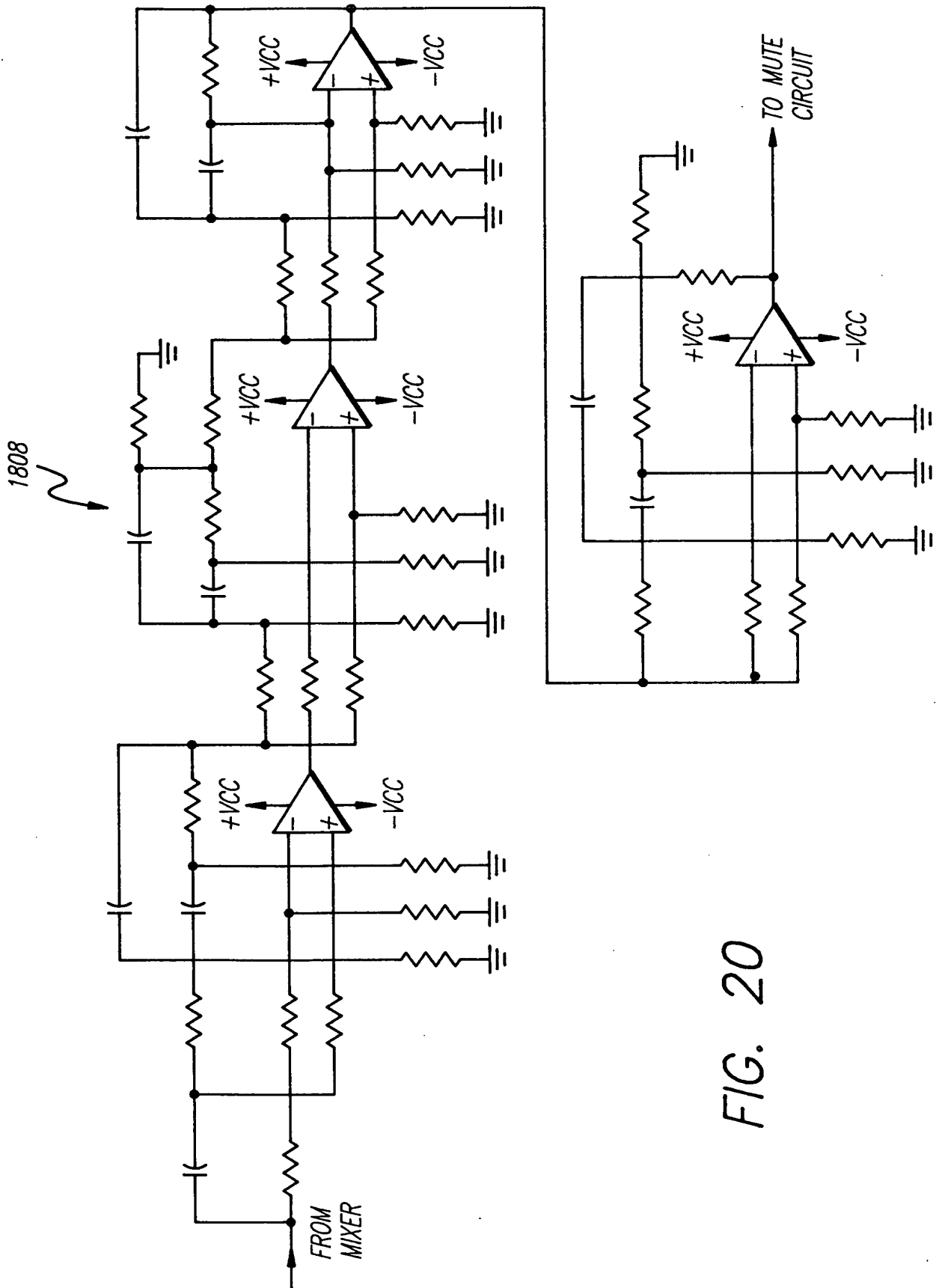


FIG. 20



FIG. 21

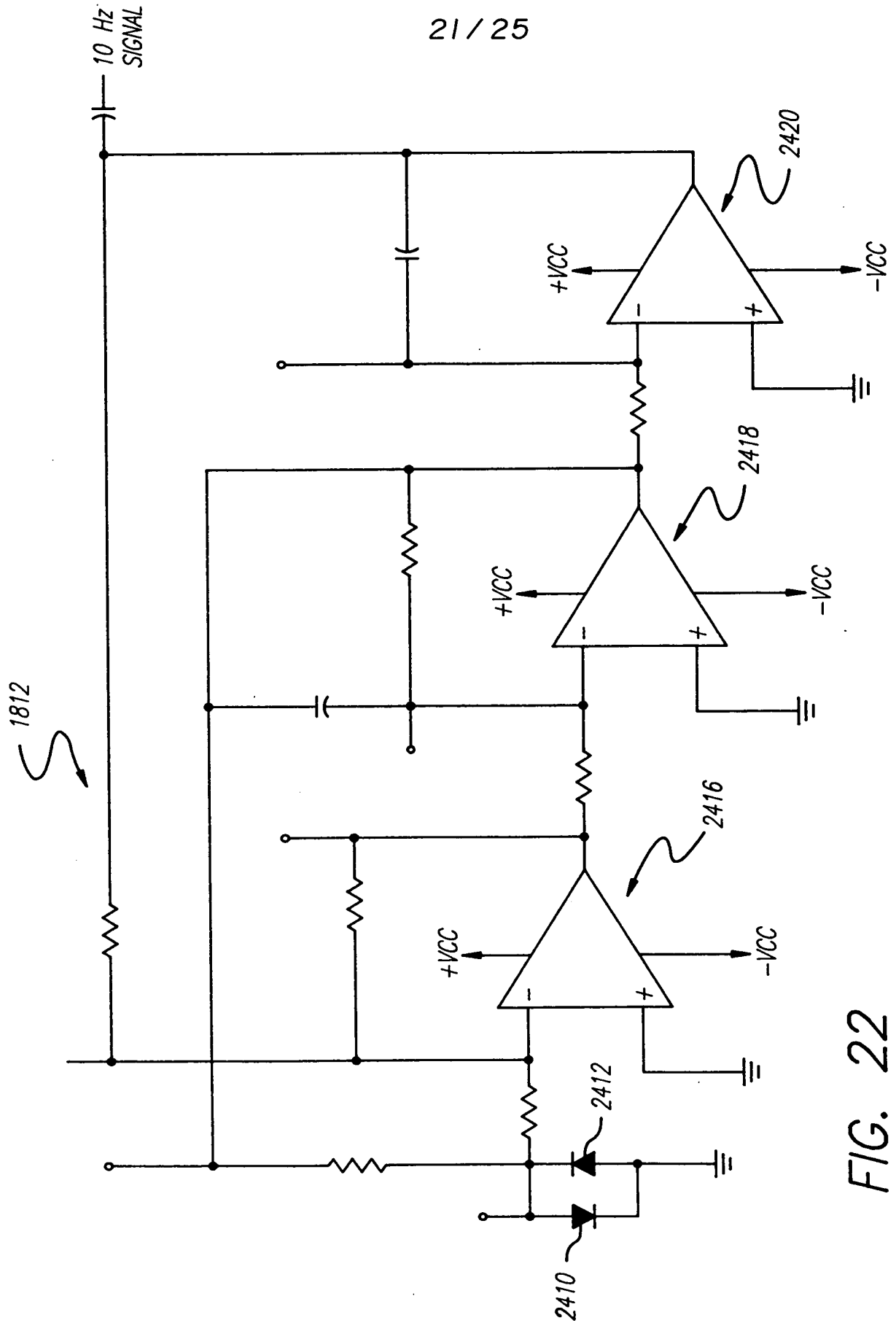


FIG. 22

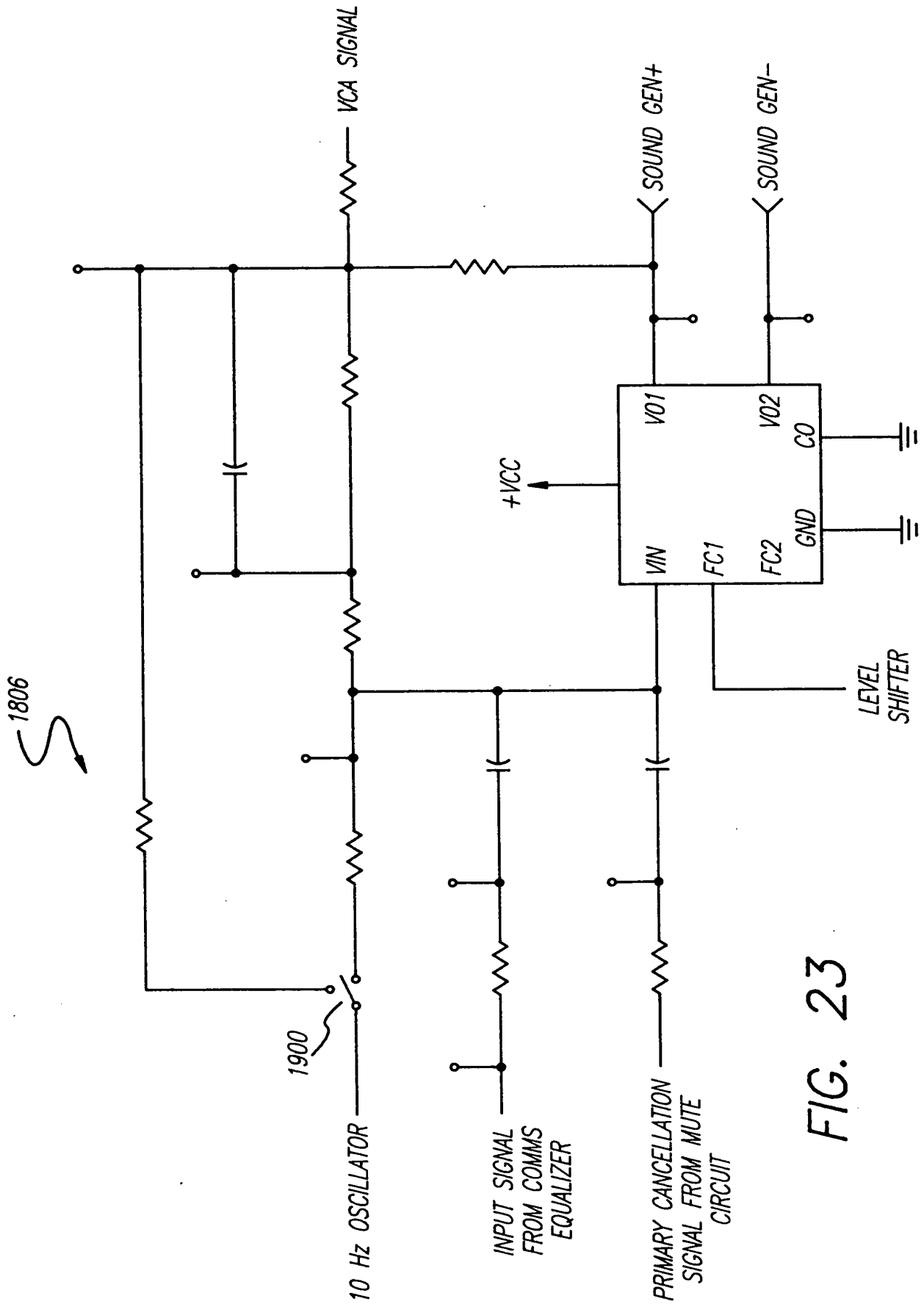


FIG. 23

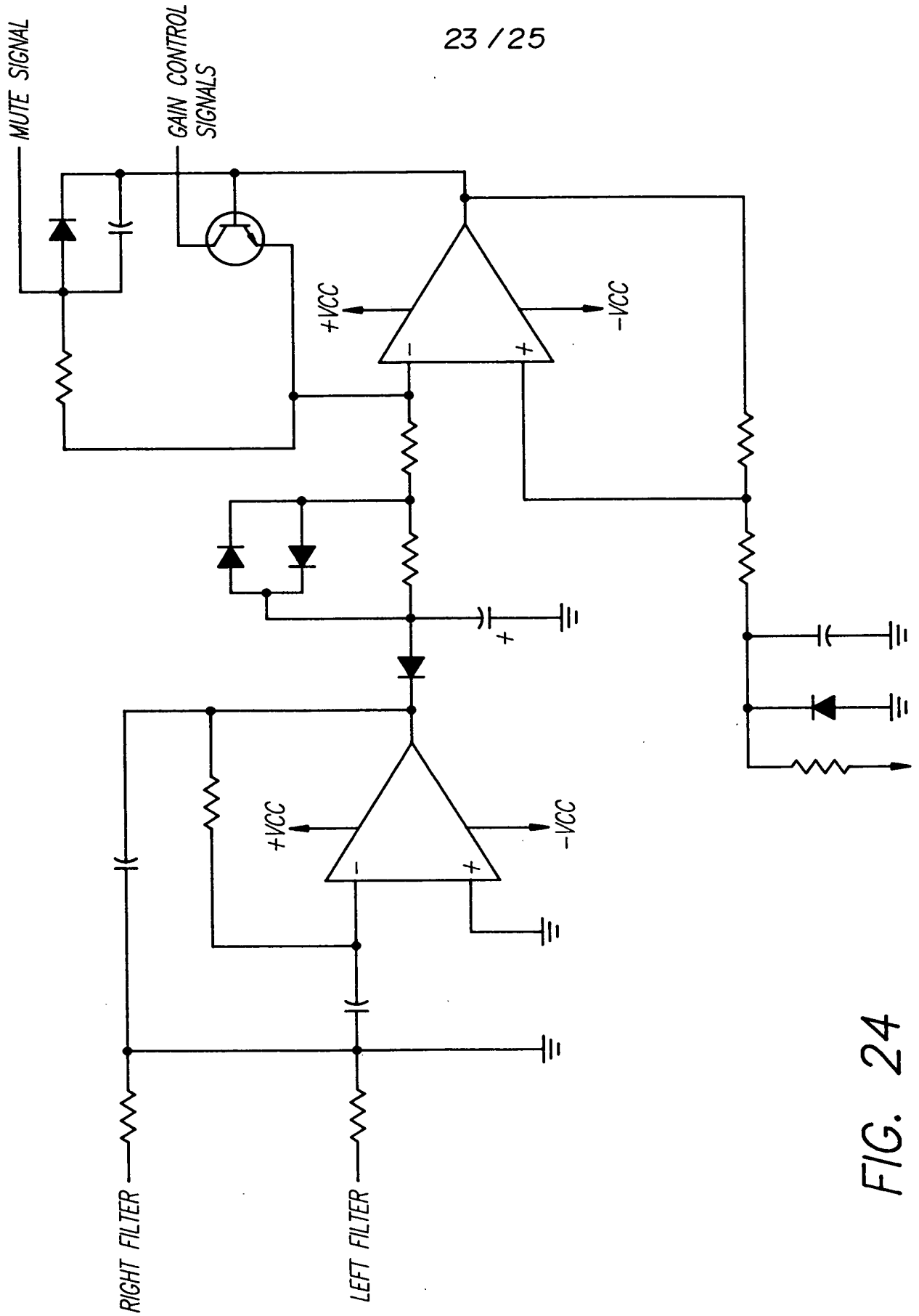


FIG. 24

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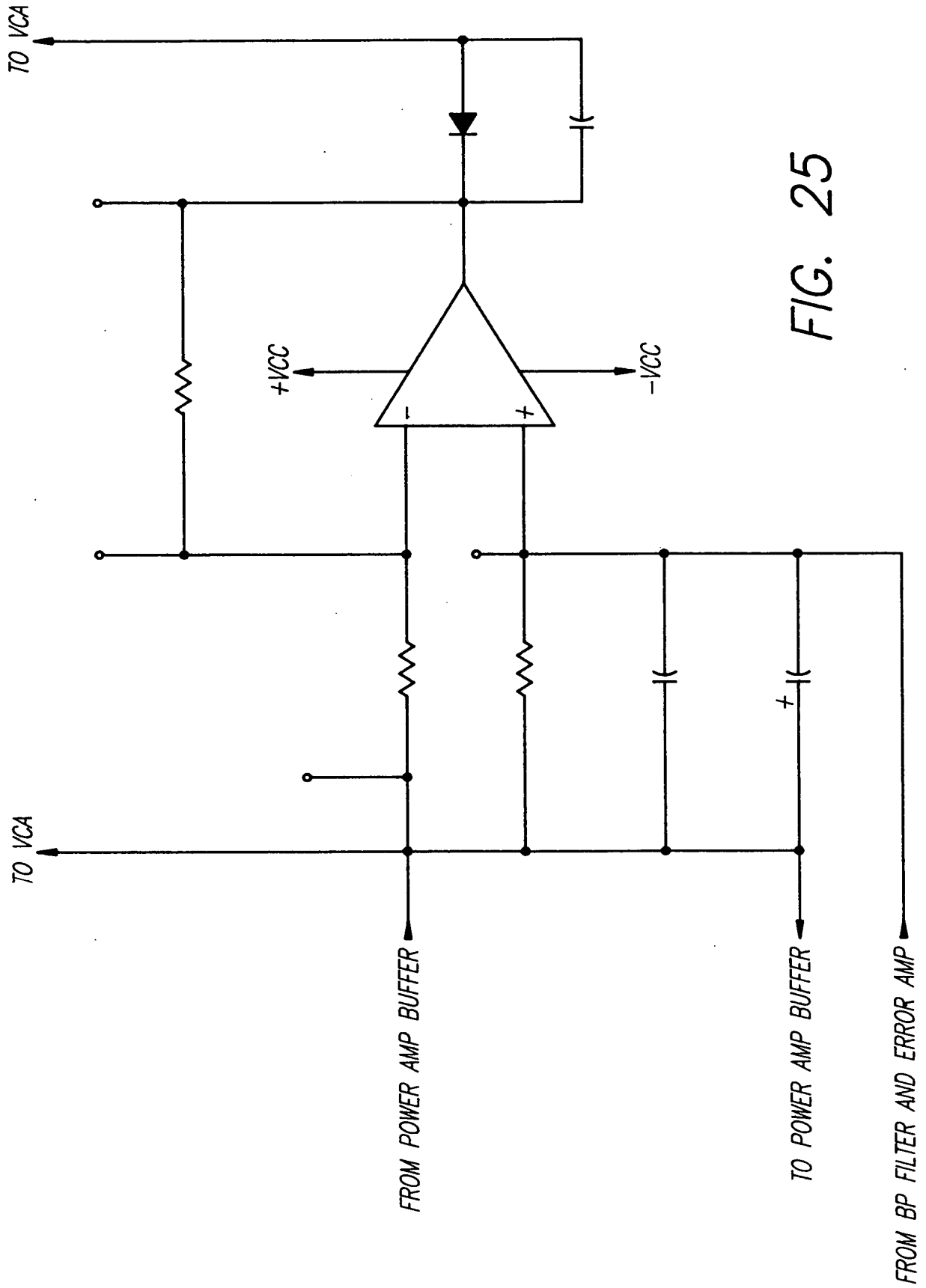
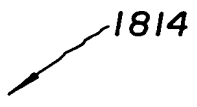


FIG. 25





**FIG. 26**